Run on:

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096229 plasmodium 09083 drosophila 06225 caenorhabdi 01796 caenorhabdi 076119 caenorhabdi 090417 ateline her 09143 plasmodium 091435 caenorhabdi 092469 arabidopsis P9127 caenorhabdi 09164 plasmodium 09547 caenorhabdi 09548 arabidopsis 09548 arabidopsis 09548 arabidopsis 09164 plasmodium 09547 caenorhabdi 09548 arabidopsis 09558 arabid
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Q17909 caenorhabdi
Q960c4 drosophila
Q9vb74 drosophila
                                                     Q06166 plasmodium
Q9srdl arabidopsis
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Q22944 caenorhabdi
                                                                                                            plasmodium
caenorhabdi
                   caenorhabdi
caenorhabdi
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Q9u0n1 plasmodium
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FES-2001 (TrEMBLrel. 19, Last annotation update)
ANNEXIN V-BINDING PROTEIN (ABP-7) (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Obsawa K., Imai Y., Ito D., Kohsaka S.;
"Molecular cloning and characterization of annexin V-binding proteins with highly hydrophilic peptide structure.";
J. Neurochem. 67:89-97(1996).
EMBL; D64061; BAA13937.1;
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26494 MW; 01BF5910ABE587F5 CRC64;
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Q960C4
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SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-BRAIN;
MEDLINE-96301899; PubMed-8667030;
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Best Local Similarity
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09lw95 nicotiana t
09lw95 drosophila
09nh7 drosophila
09nh7 drosophila
09fxb5 arabidopsis
09fxb5 arabidopsis
09fxq arabidopsis
09srel arabidopsis
09syq4 arabidopsis
                                                                                                                        ; Search time 30.15 Seconds
(without alignments)
1663.964 Million cell updates/sec
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098rd2 arabidopsis
098rp6 arabidopsis
096911 fugu rubrip
096127 plasmodium
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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Q9SYP6
Q9DGL1
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Q9W6Q4
Q9LW95
Q9VZP5
Q9NJH7
Q18F01
Q9FXB5
Q9FXB5
Q9SRE1
Q9SRE1
Q93YQ4
Q95XW8
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Result Š 2

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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last ennotation update)
0STEOBLAST TRANSLATION FACTOR 3F (INITIATION OF TRANSLATION FACTOR 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 KSNKKWDGSEEDEDNSKKIKERSRINSSGESGDESDEFLQSRKGQKKNQKNKPGPNIESG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 DEEEESSFKVKTVAQKKAEKKRERERKKREEEEKAKLRKLKEKEELE-GGKEAAKPKEAPKK 387
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                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                       NEQUENCE FROM N.A.
Weber J.A., Gay C.V.;
Weber J.A., Gay C.V.;
"Cloning of novel cDNAs from chicken osteoblasts by homology to the sodium-calcium exchanger.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF144637; AAD31321.1;
EMBL; AJ277602; CAB89284.1; -.
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SEQUENCE FROM N.A.
Weber J.A., Stains J.P., Gay C.V.;
"Identification of novel CONAS from cultured chick osteoblasts
                                                   181 VLVLRGIPDAGA--ASEEKGDIAATLEDDNEGDKKKKDKKKKTEKDDKEKEKKG
                                       194 TVKSKVTVDTGVIPASEEKAETPTAAEDDNEGDKKKKDKKKKKGEKEEKEKKKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.0%; Score 792; DB 13; Length 655; 44.1%; Pred. No. 1.9e-35; Live 24; Mismatches 55; Indels 16
                                                                                                                                                                                                                                                                                                                                                    similarity to the sodium-calcium exchanger.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
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74483 MW; DC33D9B4CDDEC5CF CRC64;
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Matches 193; Conserv
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192 - EETVKSKVTVDTGVIPASEEKAETPTAAEDDNEGDKKKKKDKKKKKGEKEEKEKKKGP 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 KESDEEDERQTEEEENDEKGVKKDKEKKNKEKKE----KKDNEKKDKS-KEETEEEKDDE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 KAEKKERERK-----KRDEE-KAKLRKLKEKEEL---ETGKKDQSKQKESQRKFE--- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hara K., Yagi M., Koizumi N., Kusano T., Sano H.; "Screening of wound-responsive genes identifies an immediate-early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 KGEKKDKEKKCKKNKKEKKDKETKDKSKEVSDEEEEKDDEEGEKKDKKKKHNKDKKETKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSSGESG-----DESDEFLQSRKGQKKNQKNKPGPNIESGNEDDDASFKIKTVAQK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 KTAKPKVEMYSGSDDDDDFNKLPKKAKGKAQKSNK----KWDGSEEDEDNSKKIKERSRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed gene encoding a highly charged protein in mechanically wounded tobacco plants.";
Plant Cell Physiol. 41:684-691(2000).
EMBL; ABO09883; BAA95789-11.
SEQUENCE 513 AA, 61019 MW; F95998A37A840B970 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CG10840 PROTEIN.
CIF2 OR CG10840.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 513;
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                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%; Score 327; DB 10; 30.2%; Pred. No. 1.3e-10; ive 57; Mismatches 102;
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                                                                                                                                                                  513 AA
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                                                                                                                                                                                                                          Created)
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum (Common tobacco).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=LEAF;
MEDLINE=20399434; PubMed=10945337;
                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
623 AKREEEERIRRLEELEAK 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 30.2%
Matches 101; Conservative
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                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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EMBL, AF143207; AAF36532.1; -. FlyBase, FBgn0026259; CIF2. InterPro; IPR000795; GTP_EFTU.
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PRINTS; PR00315; ELONGATNFCT.
                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Cell 5:181-187(2000).
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Matches 92; Conservative
                                                                                                                                                                                                                                         PRELIMINARY;
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DERE 336
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                                                                                                                                                                                                                                                                                                                                                                     PROTEIN
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                                                                                                                                               RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gocaye R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
Ratton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Randon R.C., Boaxer E.G., Helt G., Change M., Pfeliffer B.D.,
RA Batlay R.M., Basu A. Rasendale J., Bayraktarolon C.R., Mikhoo G.L.G.,
RA Beson K.Y. Bancs P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Bancs P.V., Burlar H., Cadlou E., Center A., Chandra I.,
R. Bortchan M.R., Boulck J., Brokstein P., Brottier P.,
R. Bortchan M.R., Boulck J., Brokstein P., Brottier P.,
R. Burlis R.M., Cavis S., Dalike C., Davenport L.B., Davies P.,
R. Burlis R., Coup E.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R. Anderin R.J., Rayleits A., Gong F. Gorrell J.H., Galser K.,
R. Anderin M.J., Harvey D., Helman T.J., Hernandez J.R., Harris M.L.,
R. Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Honck J.,
R.A. Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Honck J.R.,
A lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lu X., Mattel B., Morincoh T.C., McLenandez J.R., Howley B.,
R. Hostin D., Houston K.A., Nixon K., Nusskern D.M., Nelson D.L.,
R.A. Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R. Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R. Luston D.R., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
R.A. Shue B.C., Siden-Klamos I. Simpson M., Stupski M.P., Smith T.,
R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
R. Shiews R., Wooder Y. C., Wu D., Yang G., Zhoo O., Zheng I.,
R. Watters R., Wooder Y. C., Wu D., Yang S., Smith R., Stener S., Robones Sequence of Drosophila melanogaster.", Smith R. Schones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 GOKKNOKNYPGPNI--ESGNEDDDASFKIKTVAQKKAEKKERERKKRDEEKAKLRKLKEK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 EELETGKKDQSKQKESQRKFEEETVKSKVTVDTGVIPASEEKAETPTAAEDDNËGDKKKK 230
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 OKIKKRKDRRAKKOSF----DDNDSEELEDKDSKSKKTAKPKVEMYSGSDDDDFNKLPK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP-binding; Protein biosynthesis.
SEQUENCE 932 AA; 102828 MW: 3899C68FF38ED23F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.6%; Score 317.5; DB 5; 30.9%; Pred. No. 6.9e-10; tive 61; Mismatches 88;
                                                                                                                                          MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR000795; GTP_EFTU.
InterPro: IPR004161; GTP_EFTU_D2.
Pfam: PF00009; GTP_EFTU_D1.
Pfam: PF03144; GTP_EFTU_D2: 1.
PRINTS; PR00315; ELONGATNFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003478; AAF47774.1;
FlyBase; FBgn0026259; CIF2.
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Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 KKLNVKGKGKAGKNDDSDEEEVVPAKGKASKKSAFELLMDDDEQDEPAAQESQSEEEEKV 119
235 QKAATEPKPKPVEKPAP---EPEPVATE-----EVQPAAEE-------EEKSSKNKKK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "VASA mediates translation through interaction with a Drosophila yIF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 FLQSRKGQKKNQKNKPGPNI--ESGNEDDDASFKIKTVAQKKAEKKERERKKRDEEKAKL 164
                                                                           231 DKKKKKGEKEEKEKE-KKKGPSKATVKAMQEALAKLKEEEERQKREEEERIKRLEELE 287
                                                                                                      279 GKKDKKAEPEEEKKDAKKKGMSASMVAAMQEQLRKRKEEEERLEREEAERIRLEDERE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 FNKLPKKAKGKACKSNKKWDGSEEDEDNSKKIKERSRINSSGESG------DESDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 RKLKEKEELETGKKDQSKQKESQRKFEEETVKSKVTVDTGVIPASEEKAETPTAAEDDNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 GDKKKKDKKKKKGEKEEKEKE-KKKGPSKATVKAMQEALAKLKEEEERQKREEEERIKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-20142670; Pubmed-10678180;
Carrera P., Johnstone O., Nakamura A., Casanova J., Jackle H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP-binding; Protein biosynthesis.
SEQUENCE 1144 AA; 127203 MW; A035415A3762CF0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 KRKDRRAKKQSFDDNDSEELEDKDSKSKKTAKPKVEMYSGSDDDDD----
                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 315; DB 5;
; Pred. No. 1.1e-09;
61; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.5%; Score 315; 30.3%; Pred. No. 1
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eudicots; Rosidae;

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Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 EEPEAEKKEEDDTEEKKKSKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 KEEEERQKREEEERIKRLEELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                               96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                       NCBI_TaxID=3702;
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9SRE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SRE1
                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AKLRKLKEK-----EELETGKKDQSKQKESQRKFEEETVKSKVTVDTGVIPASEEKAE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 TPTAAEDDNEGDKKKKDKKKK--KGEKEEKEKKKKGPSKATVKAMQEALAKLKEEEERQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDDDD-----DFNKLPKKAKGKAQKSNKKWDGSEEDEDNSKKIKERSRINSSGESG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 DESDEFLOSRKGOKKNOKNKPGPNIESGNEDDDASFKIKTVAOKKAEKKERERKKRDEEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       NSPOKIKKRKDRRAKKQSFDDNDSEELEDKDSKSK------KTAKPKVEMYSG 50
                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                          Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                               STRAIN-BRISTOL N2;
Gatumo S., Wu X.;
"The sequence of C. elegans cosmid C33G8.";
submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                        2BFBD8E1269AA92D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
  01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 46.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                 90;
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.4%; Score 314; DB 5; Best Local Similarity 27.4%; Pred. No. 5.1e-10; Matches 85; Conservative 69; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 390 AA; 46670 MW;
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                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2001) to the EMBL; U53154; AAC25848.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                            'Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 KREEEERIKR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 DEDDKKKDKK 388
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 Waterston R.;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brssicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 EKAETPTAAEDDNEGD----KKKKDKKKKKGEKEEKEKEKKKGPSKATVKAMQEALAKL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 KGQKKNQKNKPGPNIESGNEDDDASFKIKTVAQKKAEKKERERKKRDEEKAKL-RKLKEK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 -----EELETGKK----DQSKQ-----KESQRKFEEETVKSKVTVDTGVIPASE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 DDDDDFNKLPKKAKGKAQKSNKKWDGSEEDEDNSKKIKERSRINSSGESGDESDEFLQSR 111
                                                                        ς.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KRNSPQKIKKRKDRRAKKQSFDDNDSEE-----LEDKDSKSKKTAKPKVEMYSGS 51
SEQUENCE FROM N.A.
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Nguyen M., Lam B., Southwick A., Bei, Buehler E., Chin C
Chiou J., Choi E., Dun P., Gonzalez A., Howng B., Kim C., Koo T.,
Lee J.M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
Pham P., Sakano H., Schwartz J., Shinn P., Thaveri A., Toriumi M.,
Vaysberg M., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (AUG-2000) to the BMBL/GenBank/DBBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAINCY. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu landiff., Rouling C.M., Roo, H., Fujii C.Y., Utterback T.R.,
Baristead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome 1 BAC F28016 genomic sequence.";
"Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC010718; AAF04435.1; -
InterPro; IPR000455; GTP_EFTU_D2.
InterPro; IPR00118; IF2.
InterPro; IPR00118; IF2.
InterPro; IPR001132; Ribosomal_L5.
Pfam; PF00009; GTP_EFTU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                          20.8%; Score 305; DB 10; Length 5 29.8%; Pred. No. 2e-09; Live 52; Mismatches 88; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE TRANSLATION INITIATION FACTOR IF-2, 35582-30916.
                                                                                                                                                                                                                                                                                              3323; AAG09099.1; -.
522 AA; 60749 MW; 09AF1853781071E5 CRC64;
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11;

Gaps

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1056 RDLKAKKKEEET(KEKKESENHKSK-----KKEDKKE-----HEDNKSMKKEEDKKE 1101
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 42.4 Kab RePIEN (FRACHENT).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                    SERVICE SESVICE SERVET 
                                                                                                                                                                                                                                                                                                                                                                 115 KKNQKNKPGPNIESGNEDDDASFKIKTVAQKKAEKKERERKKRDEEKAKLRKLKEKEELE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDLEVKESDVKVEEHEKEHKKGKEKKHEELEEEKEGKKKKNKKEKDESGPEEKNKKADKE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSRINSSGESGDESDEFLQSRKGQKKNQKNKPGPNIESGNEDDDASFKIKTVAQKKAEKK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKRNSPQKIKKRKDRRAKKQSFDDN-----DSEELEDKDSKSKKTAKPKVEMYSGSD 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 DD-------EDFNKLPKKAK------GKAQKSNKKWDGSEEDEDNSKKIKE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Chall G., Bowser L., Jones T., Bahn J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (OCT-2001) A., Davis R.W.;

EMBL, AX059831; AAL24313.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| | :|:| :|| : :| | : :| 37 VKAKSIEKVKAKKDESSGKSKKDKEKKGKKOKKDGKWSKKHEEGH
                                                                                                                                                                                                                                                                                                                                                                                                                  1012 KKEYEEK ------KSKTKEEAKKEKKKSODKKREEKDSEERKSKKEKEES
                                                                                                                                                         MKRNSPQKIKKKRDRRA---KKQSFDD-NDSEELEDKDSKSKKTAKPKVEMYSGSDDDDD
                                                                                                                                                                                                                                                          57 F -- NKLPKKAKGKAQKSNKKWDGSEEDEDNSKKIKERSRINSSGESGDESDEFLQSRKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --KKGPSKATVKAMQEALAKLKEEEERQKREEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 TGKKDQSKQKESQRKFEEETVKSKVTVDTGVIPASEEKAETPTAAEDDNEGDKKKKDKKK
                                                   Length 2081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 363;
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                                                     DB 10;
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Pred. No. 2.2e-08;
3; Mismatches 107;
                                                                              9e-08;
                                                   Score 283.5;
Pred. No. 9e-C
60; Mismatches
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                                                   19.38; 27.48;
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29.2%;
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                                                                                                      Conservative
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NON_TER 363 36
SEQUENCE 363 AA; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 KKGEKEEKEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 RIKRLEELES 288
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100; Conserv
                                                                              Similarity
                                                                                                      85;
                                                   Ouery Match
Best Local S
Matches 85,
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Best Local 3
Matches 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SNGDKDDEPVISFTGKKNASNKGKKGFAVSAFDALGGDKDDEEVDGDEEQVSPIT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEVEKVQAQPGPVAPVENAGEKEGEKETVETAAAKKKKKKKEKDKEKKAAAAATSSVEAK 357
                                                                                                                                                                                                                                                                                                                      11 MGRKKPSSSRGGDDEQPPAASSLVGAESKKKAVQSDEEDKYSINTEEEKVVITGKKKSNK 70
                                                                                                                                                                                                                                                                                     . 1 MKRNSPQKIKKRKDRR-----AKKQSF--DDNDSEELEDKDSKSKKTAKPK--V 45
                                                                                                                                                                                                                                                                                                                                                                                         EMYSGSDDDDDFNKL-----PKKAKGKAQKSNKKW---DGSEEDEDNSKKIKERSR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09LH98;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLRel. 19, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, BAC CLONE: T19N8
Arabidopsis thallana (Mouse-ear cress).
Arabidopsis thallana (Mouse-ear cress).
Spermatophyta: Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 INSSGESCDESDEFLQSRKGQKK-NQKNKPGPNIES-----GNEDDD-----AS
                                                                                                                                                                                                                                                                                                                                                                                                                    178 FSGKKTRSSKSSKKTTNKVALPDEEEGTMGDEESLEITFSGKKKGSIVLASLGDDSVADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --KAKLRKLKEKEELETGKKDOSKOKESO--RKFEEETVKSKVTVDTGVIPASEEKAET-
                                                                                                                                                                               DB 10; Length 1224;
                                                                                                                                                                                                                                     157;
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 3.1 Sequence features of the regions of 4,251,695 bp covered by TAC and BAC clones.";
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 7:217-221(2000).
EMBL; AP002057; BAB03174.1; -.
SEQUENCE 2081 AA; 232851 MW; D3603E1F85EFFF29 CRC64;
                                                   UNKNOWN_1.
Protein biosynthesis.
6C25811EB0B87002 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKIKTVAQKKAEKK------ERERKKRDEE------
                                                                                                                                                                            19.4%; Score 284.5; DB 10; 25.6%; Pred. No. 5.1e-08; Live 56; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2081 AA.
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MEDLINE-20363099; Pubmed-10907853;
                     PRINTS; PRO0315; ELONGATNFCT.
PROSTTE; PSO0356; RIBOSOMALLE;
GTP-binding; Initiation factor;
SEQUENCE 1224 AA; 135051 MW;
Pfam; PF03144; GTP_EFTU_D2; 2.
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                       Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                               Query Match
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215 TPTAAEDDNEGDKK---KKDKKKKK-
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                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                    eurosids II; Bra
NCBI_TaxID=3702;
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01-MAY-2000 (
01-DEC-2001 (
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                                                                                                                                                                                                                                        OSLGZ9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 KLPKKAKGKAQKSNKKWDGSEEDEDNSKKIKERSRINSSGESGDESDEFLQSRKGQ---- 114
                                                                                                                    251
                                                                                                                                           252 ---KKEKDES-CAEEKKKKPDKEKKEKDESTEKEDKKLKGKKGKGEKPEKEDEGKKTKEH 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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KKH-----EDVSQEKEELEEEDGKKNKKKEKD----ESGTEE-----KKKKPKKEKKQ
                                                                                                                    IPASEEKAETPTAAEDDNEGDKKKKDK-------KKKKGEKEEKEKE-KKKGPS
                                     ERERKKRDEEKAKLRKLK-EKEELETGKKDQSKQKE----SQRKFEEETVKSKVTVDTGV
                                                          80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Smith A., Wohldmann P.;
"The sequence of C. elegans cosmid Y55B1BR.";
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases:
EMBL; AR(024824; AR(85503.1; -. Hypothetical protein 
                                                                                                                                                                                                                          308 DATEQEMDDEAADHKEGKKKKKNKNKDKAKKKETVIDEVCEKETK 349
                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 77.9 KDA PROTEIN.
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                                                                                                                                                                                                   KATVKAMQEALAKLKEEEERQKREEEER----IKRLEELESK
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MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                          122 PGPNIESGNEDDDASFKIKTVAQKKAEKKERERKKRDEEKAKLRKLKEKEELETGKKDQS
                           2 KRNSPQKIKKRKDRRAKKQSFDDNDSEELEDKDSKSKKTAKPKVEMYSGSDDDDFNKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 KOKESORKFEEETVKSKVTVDTGVIPASEEKAETPTAAEDDNEGDKKKKDKKKKGEKEE
-GEKEEKEKE---KKKG--PS
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE TRANSLATION INITIATION FACTOR IF-2, 73082-68138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura Y.;
"Structural Analysis of Arabidopsis thaliana Chromosome Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002460; BAA97098.1; -. Interpro; IPR001386; Linker_histone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33307 MW; 43E2394CB8131143 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) GENOMIC DNA, CHROMOSOME 3, BAC CLONE:F1D9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.1%; Score 279.5; DB 10; 25.3%; Pred. No. 2.6e-08; Live 70; Mismatches 99;
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192 GSRRNRERERSRE------VGNEE------SDDDVKRDLKR--RRKEGGERKEKER 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 ESQRKFEEETVKSKVTVDTGVIPASEEKAETPTAAEDDNEGDKKKKDKKKKKGEKEEKEK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKKKG------PSKATVKAMQEALAKLKEEEE---RQKREEEE-----RIKRLEELE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 KSNKKWDGSEEDEDNSKKIKERSRINSSGESGDESDE----FLQSRKGQKKNQKNKPGP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIESGNEDDDASFKIKTVAQKKAEKKERERKKRDEEKAKLRKLKEKEELETGKKDQSKQK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 KKRKDRRAKKQSFDDNDSEELEDKDSKSKKTAKPKVEMYSGSDDDDDFNKLPKKAKGKAQ 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Caranthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Takifugu.

NGBI_TaxID=31033;
Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P., Gonzalez A., Kremenetskala I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskala V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (MAY 1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE. EMBL; AC007369; AAD305991; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
RETINITIS PIGMENTOSA GIPASE REGULATOR-LIKE PROTEIN (FRAGMENT).
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
ATP-binding; Helicase; RNA-binding.
SEQUENCE 1166 AA; 133033 MM; 597BD171F02666B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.5%; Score 272; DB 10; 25.5%; Pred. No. 2.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75; Mismatches
                                                                                                                                                                                                              InterPro; IPR001410; DEAD.
InterPro; IPR000629; DEAD_ATP_helicase.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                 Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pigmentosa.";
Nat. Genet. 0:0-0(2000).
EMBL; AF286475; AAG00554.1;
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                             SMART; SM00487; DEXDC; 1. SMART; SM00490; HELICC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RK 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II: Brassicales, Brassicaceae, Arabidopsis.
                                                C STRAIN-CY. COLUMBIA;

LIN X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

Maitin E., Bonning C.M., Koo H., Fujil C.Y., Utterback T.R.,

Barnatead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;

"Arabidopsis thaliana chromosome 1 BAC F28016 genomic sequence.";

"Arabidopsis thaliana chromosome 1 BAC F28016 genomic sequence.";

EMBL; ACO10718; AAF04442.1:

"InterPro: IPR000795; GTP_EFTU.

"InterPro: IPR000195; GTP_EFTU.

"InterPro: IPR000195; FTP.

"InterPro: IPR000196; FTP.

"InterPro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : : | : : | : : | | 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 KKGAQIDDDEYSIGTELSEESKVEEEKVVVITGKKKGKKGKKGUKKGTQODDDDFSDKVSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 SKKGKKGGNSFAASAFDALGSDDDDTEEVHEDEEEESPITFSGKKKKSSKSKKNTNSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 -----KPGPNIESGNED-----DDASFKIKTVAQKKAEKKE------RERKKRDEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 ADLLDEEEGTDASNSRDDENTIEDEESPEVTFSGKKKSSKKKGGSVLASVGDDSVADETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AKLRKLKEKEELETGK-KDQSKQKESQRKFEEETVKSKVTVDTGVIPAS-----EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 TS--DTKNVEVVETGKSKKKKKNNKSGRTVQEEEDLDKLLAALGETPAAERPASSTPVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAETP----TAAEDDNEGD----KKKKDKKKKKGE------KEEKEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KKKGPSKAT-----VKAMQEALAKLKEEEERQKREEEERI-----KR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---NKLP-----KKAKGKA------DKSNKKWDGSEEDE------DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKKIKE-----RSRINSSGESGDESDEFLQ-----SRKGOKKNOKN----
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length, 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 KKQSFDDNDSEELEDKDSKSKKTAKPKVEMYSG-----SDDDDDF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        18.8%; Score 276.5; DB 10; 26.0%; Pred. No. 1.4e-07; ive 59; Mismatches 100; ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 26.0°
Matches 111; Conservative
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SEQUENCE FROM N.A.
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Q9SYP6
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11;

Gaps

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                                                                                                                                                                                               183 QKESQRKFEEETVKSKVTVDTGVIPASEEKAETPTAAEDDNEGDKKKKDKKKKK----GE 238
                                                                                                                                                                                                                                                                                                                              Query Match 18.2%; Score 267.5; DB 13; Length 791; Best Local Similarity 24.1%; Pred. No. 2.9e-07; Matches 70; Conservative 84; Mismatches 118; Indels 19; Gaps
                                                                                                            14 DRRAKKQSFDDNDSEEL----EDKDSKS---KKTAKPKVEMYSGSDDDDFNKLPKKA 64
                                                                                                                                                                                                                                                                                                                                                                          239 KEEKEKEKKKGPSKATVKAMQEALAKLKEEEERQKREEEERIKRLEELESK 289
                                                                                                                                                                                                                                                                                                                                                                                          791 AA; 89672 MW; DA40A0FFA99E3E39 CRC64;
SEQUENCE
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